

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polynucleotide, which encodes a protein comprising the amino acid
5 sequence of SEQ ID NO:2.

2. The isolated polynucleotide of Claim 1, wherein said protein has OxyR
transcriptional regulator activity.

3. A vector comprising the isolated polynucleotide of Claim 1.

4. A host cell comprising the isolated polynucleotide of Claim 1.

10 5. The host cell of Claim 4, which is a *Coryneform* bacterium.

6. The host cell of Claim 4, wherein said host cell is selected from the group
consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium*
acetoacidophilum, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*,
Brevibacterium flavum, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

15 7. A method for detecting a nucleic acid with at least 70% homology to nucleotide of
Claim 1, comprising contacting a nucleic acid sample with a probe or primer comprising at
least 15 consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15
consecutive nucleotides of the complement thereof.

20 8. A method for producing a nucleic acid with at least 70% homology to nucleotide of
Claim 1, comprising contacting a nucleic acid sample with a primer comprising at least 15
consecutive nucleotides of the nucleotide sequence of Claim 1, or at least 15 consecutive
nucleotides of the complement thereof.

9. A process for screening for polynucleotides, which encode a protein having OxyR
transcriptional regulator activity comprising

25 a) hybridizing the isolated polynucleotide of Claim 1 to the polynucleotide to be
screened;

b) expressing the polynucleotide to produce a protein; and

c) detecting the presence or absence of OxyR transcriptional regulator activity in said
protein.

30 10. A method for making OxyR transcriptional regulator protein, comprising

a) culturing the host cell of Claim 4 for a duration of time under conditions suitable
for expression of OxyR transcriptional regulator protein; and

b) collecting the OxyR transcriptional regulator protein.

11. An isolated polynucleotide, which comprises SEQ ID NO:1.

12. An isolated polynucleotide, which is complimentary to the polynucleotide of Claim 11.

13. An isolated polynucleotide, which is at least 70% identical to the polynucleotide of Claim 11.

14. An isolated polynucleotide, which is at least 80% identical to the polynucleotide of Claim 11.

15. An isolated polynucleotide, which is at least 90% identical to the polynucleotide of Claim 11.

16. An isolated polynucleotide, which comprises at least 15 consecutive nucleotides of the polynucleotide of Claim 11.

17. An isolated polynucleotide, which hybridizes under stringent conditions to the polynucleotide of Claim 11; wherein said stringent conditions comprise washing in 5X SSC at a temperature from 50 to 68 C.

18. The isolated polynucleotide of Claim 11, which encodes a protein having OxyR transcriptional regulator activity.

19. A vector comprising the isolated polynucleotide of Claim 11.

20. A host cell comprising the isolated polynucleotide of Claim 11.

21. The host cell of Claim 20, which is a *Coryneform* bacterium.

22. The host cell of Claim 20, wherein said host cell is selected from the group consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

23. A process for screening for polynucleotides, which encode a protein having OxyR transcriptional regulator activity comprising

a) hybridizing the isolated polynucleotide of Claim 11 to the polynucleotide to be screened;

b) expressing the polynucleotide to produce a protein; and

c) detecting the presence or absence of OxyR transcriptional regulator activity in said protein.

24. A method for detecting a nucleic acid with at least 70% homology to nucleotide of Claim 11, comprising contacting a nucleic acid sample with a probe or primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 11, or at least 15 consecutive nucleotides of the complement thereof.

25. A method for producing a nucleic acid with at least 70% homology to nucleotide of Claim 11, comprising contacting a nucleic acid sample with a primer comprising at least 15 consecutive nucleotides of the nucleotide sequence of Claim 11, or at least 15 consecutive nucleotides of the complement thereof.

26. A method for making OxyR transcriptional regulator protein, comprising
a) culturing the host cell of Claim 20 for a duration of time under conditions suitable for expression of OxyR transcriptional regulator protein; and
b) collecting the OxyR transcriptional regulator protein.

27. A *Coryneform* bacterium, which comprises enhanced expression of the *oxyR* gene.

28. The *Coryneform* bacterium of Claim 27, wherein said *oxyR* gene comprises the polynucleotide sequence of SEQ ID NO:1.

29. *Corynebacterium glutamicum* DSM 13457.

30. *Escherichia coli* DSM 13244.

31. A process for producing L-amino acids comprising culturing a bacterial cell in a medium suitable for producing L-amino acids, wherein said bacterial cell comprises enhanced expression of the *oxyR* gene.

32. The process of Claim 31, wherein said bacterial cell is a *Coryneform* bacterium or *Brevibacterium*.

33. The process of Claim 32, wherein said bacterial cell is selected from the group consisting of *Coryneform glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

34. The process of Claim 31, wherein said *oxyR* gene comprises the polynucleotide sequence of SEQ ID NO:1.

35. The process of Claim 31, wherein said L-amino acid is L-lysine.

36. The process of Claim 31, wherein said bacteria further comprises at least one gene whose expression is enhanced, wherein said gene is selected from the group consisting of *dapA*, *gap*, *tpi*, *pgk*, *pyc*, *lysC*, *lysE*, *mgo*, *zwf*, *gnd*, *sod*, and *zwa1*.

37. The process of Claim 32, wherein said bacteria further comprises at least one gene whose expression is attenuated, wherein said gene is selected from the group consisting of *pck*, *pgi*, *poxB*, and *zwa2*.

38. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO:2.